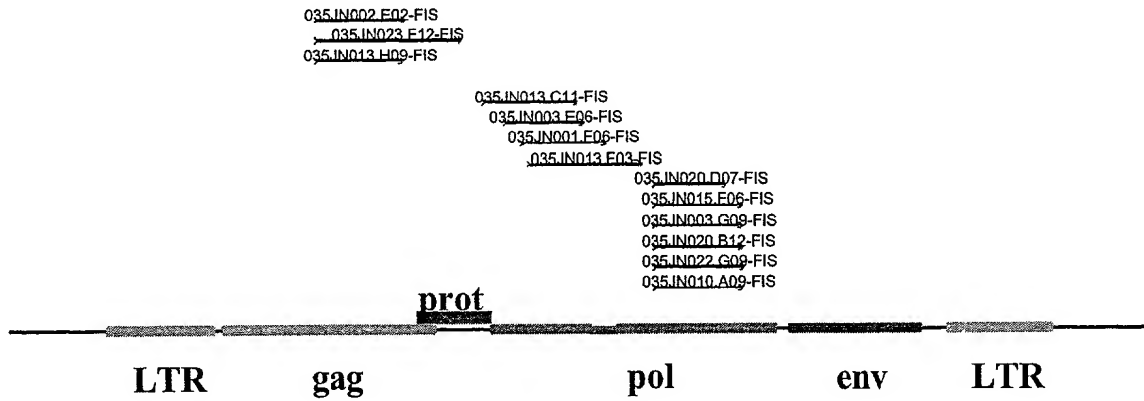
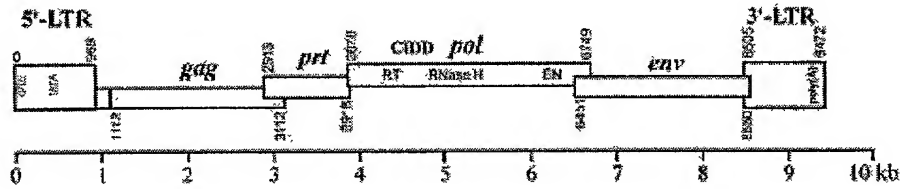
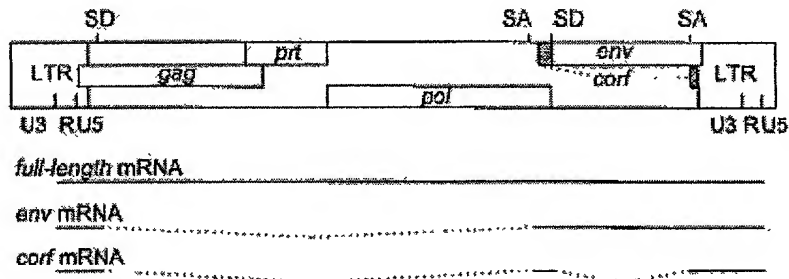
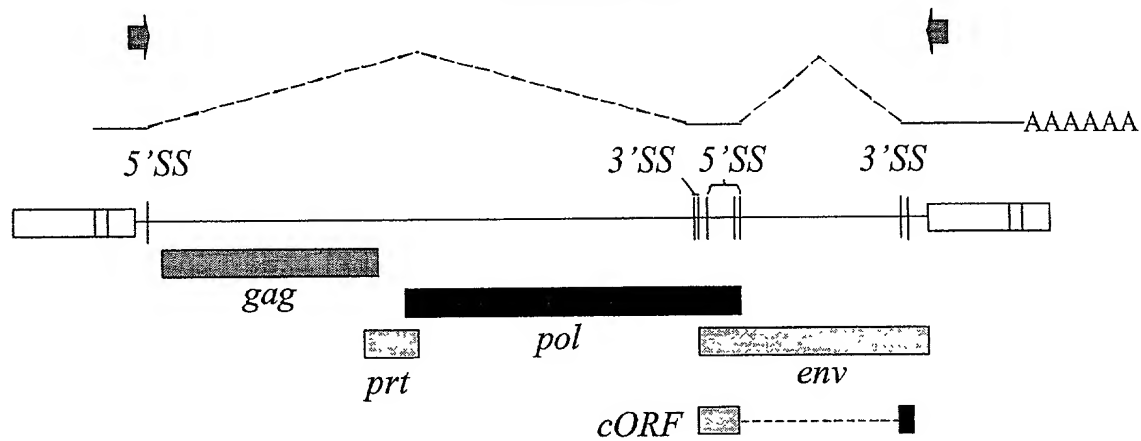


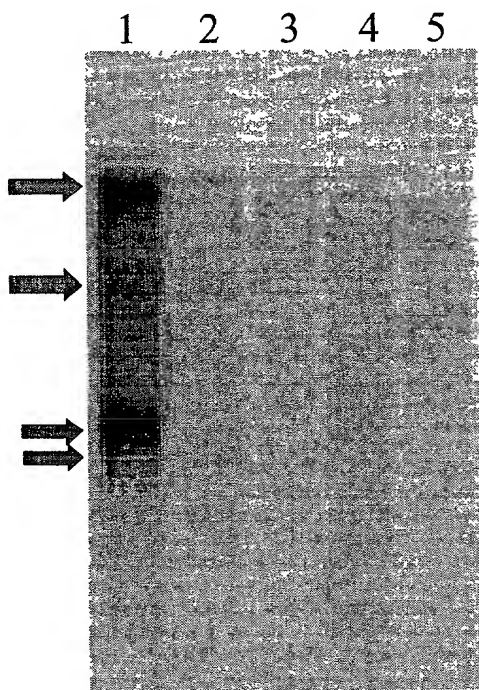
**FIGURE 1****FIGURE 2****FIGURE 3**

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**FIGURE 4**



**FIGURE 5**



**FIGURE 6**

ENV GENOMIC HERV MDA (1) ----- AGCTTTGAGTCTCTGCA  
 ENV GENOMIC HERV-K TAN. (1) ----- TGTCTTGAGTCTCTGCA  
 ENV GENOMIC AC025420 (1) ----- ACCTTTGAGTCTCTGCA  
 ENV GENOMIC AP000776 (1) ----- ACCTTTGAGTCTCTGCA  
 ENV GENOMIC HERV-K8 (1) ----- ACCTTTGAGTCTCTGCA  
 ENV GENOMIC HERV-KI (1) ----- ACCTTTGAGTCTCTGCA  
 ENV HERV-K AF023261 (1) GGGGAGAGGTTTGTCTTGTGTTTACCAGGAGAGAAATCAGCTTCTCGTTTGGATACCCACTAGCACTTTGAGTCTCTGCA  
 ENV GEN AL035086 (1) ----- ACCTTTGAGTCTCTGCA  
 ENV GENOMIC AL035587 (1) ----- ACCTTTGAGTCTCTGCA  
 ENV GENOMIC AC012068 (1) ----- ACCTTTGAGTCTCTGCA  
 ENV GENOMIC AF277315 (1) ----- ACCTTTGAGTCTCTGCA  
 ENV GENOMIC AF027650 (1) GGGGAGAGGTTTGTCTTGTGTTTACCAGGAGAGAAATCAGCTTCTCGTTTGGATACCCACTAGCACTTTGAGTCTCTGCA  
 ENV GENOMIC AC078899 (1) ----- ACCTTTGAGTCTCTGCA  
 ENV GENOMIC HERV-KII (1) ----- ACCTTTGAGTCTCTGCA  
 ENV GENOMIC AC008813 (1) ----- ATACCCACTAGCACTTTGAGTCTCTGCA  
 ENV GENOMIC AC012309 (1) ----- TAGCACTTTGAGTCTCTGCA  
 ENV GENOMIC AL121932 (1) ----- ACCTTTGAGTCTCTGCA  
 ENV GENOMIC AD000090 (1) ----- ACCTTTGAGTCTCTGCA  
 ENV GEN AL160008 (1) ----- ACCTTTGAGTCTCTGCA  
 ENV GENOMIC HEU32496 (1) ----- GGGTAAATCATTGAGGACAAAGTCGACGAGAGAGATCCCGAGGACGCTCTACAGTCAGCGCTTACCGCTTTGAGTCTCTGCA  
 ENV GENOMIC AC011467 (1) ----- GGTCTTTGCTTGTGTTTACCAGGAGAGA -AAATCAGCTTCTCGTTTGGATGCCACTAGCACTTTGAGTCTCTGCA  
 ENV GENOMIC AF235103 (1) ----- TTTTCTCTGTGTTTACCAGGAGAGA -AAATCAGCTTCTCGTTTGGATGCCACTAGCACTTTGAGTCTCTGCA  
 ENV GENOMIC AC026786 (1) ----- TTTTGTCTGTGTTTACCAGGAGAAATAAATCAGCTTCCAGTTTGGATCTTCAAACTT  
 ENV GENOMIC AC034203 (1) ----- CACCAGGAGA -AAATCAGCTTCTCGTTTGGGATGCCACTAGCACTTTGAGTCTCTGCA  
 ENV GENOMIC AC018809 (1) ----- TTTGCTTTGTTTACCAGGAGAGA -AAATCAGCTTCTCGTTTGGGATGCCACTAGCACTTTGAGTCTCTGCA  
 ENV GENOMIC HERV-KI02 AF164610 (1) ----- TTGCTTTGTTTACCAGGAGAGA -AAATCAGCTTCTCGTTTGGGATGCCACTAGCACTTTGAGTCTCTGCA  
 ENV GENOMIC FRAG. AF260253 (1) ----- ACATTGGAAGTTCTTACA  
 CONSENSUS (2) ----- ACATTGGAAGTTCTTACA

81 160

ENV GENOMIC HERV MDA (18) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC HERV-K TAN. (18) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC025420 (18) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AP000776 (18) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC HERV-K8 (1) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC HERV-KI (18) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV HERV-K AF023261 (81) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GEN AL035086 (1) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AL035587 (18) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC012068 (6) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AF277315 (15) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AF027650 (79) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC078899 (16) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC HERV-KII (18) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC008813 (29) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC012309 (21) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AL121932 (18) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AD000090 (18) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GEN AL160008 (1) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC HEU32496 (78) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC011467 (74) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AF235103 (72) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC026786 (58) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC034203 (58) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC018809 (16) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC HERV-KI02 AF164610 (70) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC FRAG. AF260253 (1) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 CONSENSUS (81) ATGAACCCATC GAGATGCAAGAGAA AGC CTCC CGGAGACGAAACCCGCAATCGAGCA C

161 240

ENV GENOMIC HERV MDA (72) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC HERV-K TAN. (83) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC025420 (83) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AP000776 (83) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC HERV-K8 (15) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC HERV-KI (83) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV HERV-K AF023261 (146) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GEN AL035086 (1) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AL035587 (83) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC012068 (71) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AF277315 (80) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AF027650 (144) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC078899 (81) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC HERV-KII (72) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC008813 (104) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC012309 (86) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AL121932 (83) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AD000090 (88) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GEN AL160008 (1) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC HEU32496 (143) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC011467 (128) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AF235103 (142) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC026786 (58) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC034203 (123) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC AC018809 (70) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC HERV-KI02 AF164610 (124) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 ENV GENOMIC FRAG. AF260253 (1) ----- GTTGAATCTCTGAGATGCAAGAGAA  
 CONSENSUS (161) T GACTCACAAGATGAA AAAATGGTGA TCAGAAGACAGATGAAGTTGCCATCCACCAAGAA GC

## FIGURE 6 CONTD...

ENV GENOMIC HERV MDA	(139)	241	320
ENV GENOMIC HERV-K TAN.	(155)	GTTCGATTAAGGCACTTAAGAGCTTACAGCTAGCTTAAGAAAAGCTTASAGATTTAAAGTTGACACCA	
ENV GENOMIC AC025420	(152)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AP000776	(155)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC HERV-K8	(87)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC HERV-KI	(155)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV HERV-K AF023261	(218)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GEN AL035086	(1)	-----	
ENV GENOMIC AL035587	(155)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC012068	(143)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AF277315	(152)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AF027650	(216)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC078899	(153)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC HERV-KII	(72)	-----	
ENV GENOMIC AC008813	(176)	ATTCGATTAAGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC012309	(154)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AL121932	(155)	ATTCGATTAAGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AD000090	(168)	ATTCGATTAAGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GEN AL160008	(34)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC HEU32496	(212)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC011467	(128)	-----	
ENV GENOMIC AF235103	(214)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC026786	(91)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC034203	(195)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC018809	(70)	-----	
ENV GENOMIC HERV-KI02 AF164610	(124)	-----	
ENV GENOMIC FRAG. AF260253	(1)	-----	
CONSENSUS	(241)	GCCTGCGACTTGGGCACAA TAAAGAGCTGACACAGTTAGCTA AAAA CT GAGAACACAAAGGTGACACAAA	
ENV GENOMIC HERV MDA	(219)	321	400
ENV GENOMIC HERV-K TAN.	(232)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC025420	(229)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AP000776	(232)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC HERV-K8	(163)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC HERV-KI	(232)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV HERV-K AF023261	(295)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GEN AL035086	(18)	-----	
ENV GENOMIC AL035587	(232)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC012068	(220)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AF277315	(229)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AF027650	(294)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC078899	(231)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC HERV-KII	(72)	-----	
ENV GENOMIC AC008813	(252)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC012309	(231)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AL121932	(232)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AD000090	(245)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GEN AL160008	(111)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC HEU32496	(289)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC011467	(128)	-----	
ENV GENOMIC AF235103	(291)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC026786	(169)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC034203	(272)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC018809	(70)	-----	
ENV GENOMIC HERV-KI02 AF164610	(124)	-----	
ENV GENOMIC FRAG. AF260253	(1)	-----	
CONSENSUS	(321)	CTCCAGAGA TATGCTGCTTGCAGCTTTGATGATTGATCAATGGTGGTAAAGTCTCCC ATGCTGTCAGGAGCAGCTGCA	
ENV GENOMIC HERV MDA	(299)	401	480
ENV GENOMIC HERV-K TAN.	(312)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC025420	(309)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AP000776	(312)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC HERV-K8	(242)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC HERV-KI	(312)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV HERV-K AF023261	(375)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GEN AL035086	(98)	-----	
ENV GENOMIC AL035587	(312)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC012068	(300)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AF277315	(309)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AF027650	(374)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC078899	(311)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC HERV-KII	(72)	-----	
ENV GENOMIC AC008813	(332)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC012309	(311)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AL121932	(310)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AD000090	(325)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GEN AL160008	(191)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC HEU32496	(369)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC011467	(128)	-----	
ENV GENOMIC AF235103	(371)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC026786	(249)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC034203	(352)	CCCGCAGCTTGGGCACTTAAGAGAGCTGAGGAGTTAGCTTAAGAAATA---TTTACGACACACAACTTTGACACAA	
ENV GENOMIC AC018809	(70)	-----	
ENV GENOMIC HERV-KI02 AF164610	(124)	-----	
ENV GENOMIC FRAG. AF260253	(1)	-----	
CONSENSUS	(401)	GCTAA TATAC TACTGGGCTATGTGCTTTCCGCCCTTAATTTGGGCGTACATGGATGGATAATCTTATGAAGT	

**FIGURE 6 CONTD...**

[illegible]



## FIGURE 6 CONTD...

ENV GENOMIC HERV MDA	(609)	-----	721	800
ENV GENOMIC HERV-K TAN.	(630)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AC025420	(627)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AP000776	(630)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC HERV-K8	(291)	-----		
ENV GENOMIC HERV-KI	(630)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV HERV-K AF023261	(693)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GEN AL035086	(416)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AL035587	(630)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AC012068	(618)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AF277315	(627)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AF027650	(692)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AC078899	(629)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC HERV-KII	(338)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AC008813	(650)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AC012309	(629)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AL121932	(627)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AD000090	(643)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GEN AL160008	(482)	-----		
ENV GENOMIC HEU32496	(441)	-----		
ENV GENOMIC AC011467	(394)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AF235103	(688)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AC026786	(564)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AC034203	(670)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC AC018809	(337)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC HERV-KI02 AF164610	(390)	GGGTAATATTATTACAGGACCTTCTTCTCAAGATCATTAATGAGCTTACCGGAGGCTTCCGACGGAAT		
ENV GENOMIC FRAG. AF260253	(1)	-----		
CONSENSUS	(721)	C GGTAAAT ATTACA GACTTTTCTTATCAAGATCATTAAATTAG CTTAAAGGGAACCTTGCCCCAGGAAT		
ENV GENOMIC HERV MDA	(685)	-----	801	880
ENV GENOMIC HERV-K TAN.	(710)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AC025420	(707)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AP000776	(710)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC HERV-K8	(291)	-----		
ENV GENOMIC HERV-KI	(710)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV HERV-K AF023261	(701)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GEN AL035086	(496)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AL035587	(710)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AC012068	(698)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AF277315	(707)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AF027650	(700)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AC078899	(709)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC HERV-KII	(418)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AC008813	(729)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AC012309	(709)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AL121932	(707)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AD000090	(723)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GEN AL160008	(543)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC HEU32496	(441)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AC011467	(474)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AF235103	(768)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AC026786	(644)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AC034203	(750)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC AC018809	(417)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC HERV-KI02 AF164610	(470)	CCCAAGGATCAAAAGGCCAGAGGCTTACTCTGGCGGAGATGCTGTATCTGGCTG TACGACAAACAT		
ENV GENOMIC FRAG. AF260253	(1)	-----		
CONSENSUS	(801)	TCCCAAG ATCAAAA A CAGAAGTTTATGTTGGAGAGATGTGTGGC AATAGTGC GTGATATTACAAACAATG		
ENV GENOMIC HERV MDA	(764)	-----	881	960
ENV GENOMIC HERV-K TAN.	(790)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ACCTGATA
ENV GENOMIC AC025420	(787)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AP000776	(790)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC HERV-K8	(291)	-----		
ENV GENOMIC HERV-KI	(790)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV HERV-K AF023261	(701)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GEN AL035086	(576)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AL035587	(790)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AC012068	(778)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AF277315	(787)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AF027650	(700)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AC078899	(789)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC HERV-KII	(498)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AC008813	(809)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AC012309	(789)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AL121932	(787)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AD000090	(803)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GEN AL160008	(623)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC HEU32496	(441)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AC011467	(554)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AF235103	(848)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AC026786	(724)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AC034203	(830)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC AC018809	(497)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC HERV-KI02 AF164610	(550)	AAATTGAACCTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA		ATCTGATA
ENV GENOMIC FRAG. AF260253	(1)	-----		
CONSENSUS	(881)	AATTGGAACTATTATAGATGCTGCTCCCTTCAAGGATTTATTTATTA CACA		ATTGC CA

## FIGURE 6 CONTD...

ENV GENOMIC HERV MDA	(820)	961	1040
ENV GENOMIC HERV-K TAN.	(846)	-----	-----
ENV GENOMIC AC025420	(843)	-----	-----
ENV GENOMIC AP000776	(846)	-----	-----
ENV GENOMIC HERV-K8	(291)	-----	-----
ENV GENOMIC HERV-KI	(846)	-----	-----
ENV HERV-K AF023261	(701)	-----	-----
ENV GEN AL035086	(632)	-----	-----
ENV GENOMIC AL035587	(870)	-----	-----
ENV GENOMIC AC012068	(834)	-----	-----
ENV GENOMIC AF277315	(843)	-----	-----
ENV GENOMIC AF027650	(700)	-----	-----
ENV GENOMIC AC078899	(845)	-----	-----
ENV GENOMIC HERV-KII	(554)	-----	-----
ENV GENOMIC AC008813	(865)	-----	-----
ENV GENOMIC AC012309	(845)	-----	-----
ENV GENOMIC AL121932	(843)	-----	-----
ENV GENOMIC AD000090	(859)	-----	-----
ENV GEN AL160008	(647)	-----	-----
ENV GENOMIC HEU32496	(441)	-----	-----
ENV GENOMIC AC011467	(610)	-----	-----
ENV GENOMIC AF235103	(904)	-----	-----
ENV GENOMIC AC026786	(780)	-----	-----
ENV GENOMIC AC034203	(886)	-----	-----
ENV GENOMIC AC018809	(553)	-----	-----
ENV GENOMIC HERV-KI02 AF164610	(606)	-----	-----
ENV GENOMIC FRAG. AF260253	(1)	-----	-----
CONSENSUS	(961)	GG CAAACTCA TC TGTCC AG GCACAG	AGTCCAGCTGTTGATAG GACTTACACAGAAAT T
ENV GENOMIC HERV MDA	(900)	1041	1120
ENV GENOMIC HERV-K TAN.	(914)	-----	-----
ENV GENOMIC AC025420	(911)	-----	-----
ENV GENOMIC AP000776	(914)	-----	-----
ENV GENOMIC HERV-K8	(291)	-----	-----
ENV GENOMIC HERV-KI	(914)	-----	-----
ENV HERV-K AF023261	(701)	-----	-----
ENV GEN AL035086	(700)	-----	-----
ENV GENOMIC AL035587	(950)	-----	-----
ENV GENOMIC AC012068	(914)	-----	-----
ENV GENOMIC AF277315	(923)	-----	-----
ENV GENOMIC AF027650	(700)	-----	-----
ENV GENOMIC AC078899	(913)	-----	-----
ENV GENOMIC HERV-KII	(622)	-----	-----
ENV GENOMIC AC008813	(933)	-----	-----
ENV GENOMIC AC012309	(913)	-----	-----
ENV GENOMIC AL121932	(911)	-----	-----
ENV GENOMIC AD000090	(927)	-----	-----
ENV GEN AL160008	(647)	-----	-----
ENV GENOMIC HEU32496	(441)	-----	-----
ENV GENOMIC AC011467	(676)	-----	-----
ENV GENOMIC AF235103	(984)	-----	-----
ENV GENOMIC AC026786	(860)	-----	-----
ENV GENOMIC AC034203	(966)	-----	-----
ENV GENOMIC AC018809	(621)	-----	-----
ENV GENOMIC HERV-KI02 AF164610	(674)	-----	-----
ENV GENOMIC FRAG. AF260253	(1)	-----	-----
CONSENSUS	(1041)	AGAC AA T A TA AA TTA A TC TCTA CC TGG AATGGGG GAAAA GGAAT TC C	
ENV GENOMIC HERV MDA	(967)	1121	1200
ENV GENOMIC HERV-K TAN.	(984)	-----	-----
ENV GENOMIC AC025420	(981)	-----	-----
ENV GENOMIC AP000776	(984)	-----	-----
ENV GENOMIC HERV-K8	(291)	-----	-----
ENV GENOMIC HERV-KI	(984)	-----	-----
ENV HERV-K AF023261	(701)	-----	-----
ENV GEN AL035086	(770)	-----	-----
ENV GENOMIC AL035587	(1017)	-----	-----
ENV GENOMIC AC012068	(981)	-----	-----
ENV GENOMIC AF277315	(990)	-----	-----
ENV GENOMIC AF027650	(700)	-----	-----
ENV GENOMIC AC078899	(993)	TTCCAGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCTTAACCTCAGCATTTCCGGGTTTCACCTTTTCCTGTTCCCA	
ENV GENOMIC HERV-KII	(692)	-----	-----
ENV GENOMIC AC008813	(1003)	-----	-----
ENV GENOMIC AC012309	(983)	-----	-----
ENV GENOMIC AL121932	(981)	-----	-----
ENV GENOMIC AD000090	(997)	-----	-----
ENV GEN AL160008	(647)	-----	-----
ENV GENOMIC HEU32496	(441)	-----	-----
ENV GENOMIC AC011467	(683)	-----	-----
ENV GENOMIC AF235103	(1051)	-----	-----
ENV GENOMIC AC026786	(927)	-----	-----
ENV GENOMIC AC034203	(1033)	-----	-----
ENV GENOMIC AC018809	(691)	-----	-----
ENV GENOMIC HERV-KI02 AF164610	(744)	-----	-----
ENV GENOMIC FRAG. AF260253	(1)	-----	-----
CONSENSUS	(1121)	-----	-----

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## FIGURE 6 CONTD...

	1201	1280
ENV GENOMIC HERV MDA	(967)	-----
ENV GENOMIC HERV-K TAN.	(984)	-----
ENV GENOMIC AC025420	(981)	-----
ENV GENOMIC AP000776	(984)	-----
ENV GENOMIC HERV-K8	(291)	-----
ENV GENOMIC HERV-KI	(984)	-----
ENV HERV-K AF023261	(701)	-----
ENV GEN AL035086	(770)	-----
ENV GENOMIC AL035587	(1017)	-----
ENV GENOMIC AC012068	(981)	-----
ENV GENOMIC AF277315	(990)	-----
ENV GENOMIC AF027650	(700)	-----
ENV GENOMIC AC078899	(1073)	CCACCCCGACTAACGCACATGCCCACTAGGGCGTGTCACACTCAGAAGTGTGAAACTCAACCGATCCCGCCCTAACCCOG
ENV GENOMIC HERV-KII	(692)	-----
ENV GENOMIC AC008813	(1003)	-----
ENV GENOMIC AC012309	(983)	-----
ENV GENOMIC AL121932	(981)	-----
ENV GENOMIC AD000090	(997)	-----
ENV GEN AL160008	(647)	-----
ENV GENOMIC HEU32496	(441)	-----
ENV GENOMIC AC011467	(683)	-----
ENV GENOMIC AF235103	(1051)	-----
ENV GENOMIC AC026786	(927)	-----
ENV GENOMIC AC034203	(1033)	-----
ENV GENOMIC AC018809	(691)	-----
ENV GENOMIC HERV-KI02 AF164610	(744)	-----
ENV GENOMIC FRAG. AF260253	(1)	-----
CONSENSUS	(1201)	-----

	1281	1360
ENV GENOMIC HERV MDA	(967)	-----
ENV GENOMIC HERV-K TAN.	(984)	-----
ENV GENOMIC AC025420	(981)	-----
ENV GENOMIC AP000776	(984)	-----
ENV GENOMIC HERV-K8	(291)	-----
ENV GENOMIC HERV-KI	(984)	-----
ENV HERV-K AF023261	(701)	-----
ENV GEN AL035086	(770)	-----
ENV GENOMIC AL035587	(1017)	-----
ENV GENOMIC AC012068	(981)	-----
ENV GENOMIC AF277315	(990)	-----
ENV GENOMIC AF027650	(700)	-----
ENV GENOMIC AC078899	(1153)	ACCACTTCCTCACCCAGCATCCATAAAGCGCGCTGCACCTTTGCGCACGCGTGACTTCCCTGGCGGACCACTGAACCTC
ENV GENOMIC HERV-KII	(692)	-----
ENV GENOMIC AC008813	(1003)	-----
ENV GENOMIC AC012309	(983)	-----
ENV GENOMIC AL121932	(981)	-----
ENV GENOMIC AD000090	(997)	-----
ENV GEN AL160008	(647)	-----
ENV GENOMIC HEU32496	(441)	-----
ENV GENOMIC AC011467	(683)	-----
ENV GENOMIC AF235103	(1051)	-----
ENV GENOMIC AC026786	(927)	-----
ENV GENOMIC AC034203	(1033)	-----
ENV GENOMIC AC018809	(691)	-----
ENV GENOMIC HERV-KI02 AF164610	(744)	-----
ENV GENOMIC FRAG. AF260253	(1)	-----
CONSENSUS	(1281)	-----

	1361	1440
ENV GENOMIC HERV MDA	(967)	-----
ENV GENOMIC HERV-K TAN.	(984)	-----
ENV GENOMIC AC025420	(981)	-----
ENV GENOMIC AP000776	(984)	-----
ENV GENOMIC HERV-K8	(291)	-----
ENV GENOMIC HERV-KI	(984)	-----
ENV HERV-K AF023261	(701)	-----
ENV GEN AL035086	(770)	-----
ENV GENOMIC AL035587	(1017)	-----
ENV GENOMIC AC012068	(981)	-----
ENV GENOMIC AF277315	(990)	-----
ENV GENOMIC AF027650	(700)	-----
ENV GENOMIC AC078899	(1233)	ACCGGAGAGCTCAATAAAGAAGATTTTGGCCCTCTTGTCTTGCCCTCTTGGCCTTATTGATCCAGGTGCTTTCCATTG
ENV GENOMIC HERV-KII	(692)	-----
ENV GENOMIC AC008813	(1003)	-----
ENV GENOMIC AC012309	(983)	-----
ENV GENOMIC AL121932	(981)	-----
ENV GENOMIC AD000090	(997)	-----
ENV GEN AL160008	(647)	-----
ENV GENOMIC HEU32496	(441)	-----
ENV GENOMIC AC011467	(683)	-----
ENV GENOMIC AF235103	(1051)	-----
ENV GENOMIC AC026786	(927)	-----
ENV GENOMIC AC034203	(1033)	-----
ENV GENOMIC AC018809	(691)	-----
ENV GENOMIC HERV-KI02 AF164610	(744)	-----
ENV GENOMIC FRAG. AF260253	(1)	-----
CONSENSUS	(1361)	-----

"102026" "10593001"



**FIGURE 6** *CONTD...*

[illegible]

## FIGURE 6 CONTD...

ENV GENOMIC HERV MDA	(1190)	1681	ATCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	1760
ENV GENOMIC HERV-K TAN.	(1209)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC AC025420	(1206)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC AP000776	(1209)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC HERV-K8	(291)			
ENV GENOMIC HERV-KI	(1209)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV HERV-K AF023261	(701)			
ENV GEN AL035086	(995)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC AL035587	(1242)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC AC012068	(1202)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC AF277315	(1215)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC AF027650	(700)			
ENV GENOMIC AC078899	(1549)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC HERV-KII	(913)			
ENV GENOMIC AC008813	(1228)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC AC012309	(1208)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC AL121932	(1207)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC AD000090	(1220)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GEN AL160008	(647)			
ENV GENOMIC HEU32496	(441)			
ENV GENOMIC AC011467	(883)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC AF235103	(1276)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC AC026786	(1152)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC AC034203	(1258)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC AC018809	(916)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC HERV-K102 AF164610	(969)	CCAGACCTCCCGACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC FRAG. AF260253	(1)			
CONSENSUS	(1681)	CCAGA TCCCAAACTATA	ACCTGTGCAAAATTCGAAATGTTTACCTTCATTCGATTTGACCTTTAAATTCGACAGCGGT	
ENV GENOMIC HERV MDA	(1268)	1761	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT	1840
ENV GENOMIC HERV-K TAN.	(1287)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AC025420	(1284)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AP000776	(1287)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC HERV-K8	(291)			
ENV GENOMIC HERV-KI	(1287)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV HERV-K AF023261	(701)			
ENV GEN AL035086	(1073)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AL035587	(1320)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AC012068	(1280)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AF277315	(1293)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AF027650	(700)			
ENV GENOMIC AC078899	(1627)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC HERV-KII	(991)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AC008813	(1238)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AC012309	(1288)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AL121932	(1285)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AD000090	(1298)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GEN AL160008	(647)			
ENV GENOMIC HEU32496	(441)			
ENV GENOMIC AC011467	(961)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AF235103	(1354)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AC012068	(1230)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AC034203	(1336)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC AC018809	(992)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC HERV-K102 AF164610	(1047)	ATTCTGTAGTGGAGAGCAGCGGTCTTGGATCCCTGTGTGAGGAGCGCGCTTGGAGGCTTGGCGTGGT		
ENV GENOMIC FRAG. AF260253	(1)			
CONSENSUS	(1761)	ATTCTGTCT GTGAGAGCAAGAGA GG GTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAGGC TC CCATCC TCCA		
ENV GENOMIC HERV MDA	(1348)	1841	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC	1920
ENV GENOMIC HERV-K TAN.	(1367)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AC025420	(1364)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AP000776	(1367)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC HERV-K8	(291)			
ENV GENOMIC HERV-KI	(1367)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV HERV-K AF023261	(701)			
ENV GEN AL035086	(1153)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AL035587	(1399)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AC012068	(1360)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AF277315	(1373)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AF027650	(700)			
ENV GENOMIC AC078899	(1707)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC HERV-KII	(1071)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AC008813	(1238)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AC012309	(1368)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AL121932	(1365)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AD000090	(1378)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GEN AL160008	(647)			
ENV GENOMIC HEU32496	(441)			
ENV GENOMIC AC011467	(1041)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AF235103	(1434)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AC026786	(1310)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AC034203	(1403)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC AC018809	(1072)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC HERV-K102 AF164610	(1127)	TATTTTACGAAGATTAAGAGCAATCTAACAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		
ENV GENOMIC FRAG. AF260253	(1)			
CONSENSUS	(1841)	TATTTT AC GAAGTATTAAAGG TT TAA TAGATCCAAAGATTCATTTTCTTTTATGAGGAGATTAATCC		

**FIGURE 6** *CONTD...*

[illegible]



**FIGURE 6** *CONTD...*

[illegible]

[illegible]



## FIGURE 6 CONTD...

2641 2707

ENV GENOMIC HERV MDA (2136) TATCTCTACTTAA-----

ENV GENOMIC HERV-K TAN. (2146) TTTTACTTACTTAA-----

ENV GENOMIC AC025420 (2143) TTTTACTTACTTAA-----

ENV GENOMIC AP000776 (2146) TTTTACTTACTTAA-----

ENV GENOMIC HERV-K8 (291) -----

ENV GENOMIC HERV-KI (2141) TTTTACTTACTTAA-----

ENV HERV-K AF023261 (701) -----

ENV GEN AL035086 (1931) TATCTCTACTTAA-----

ENV GENOMIC AL035587 (2146) -----

ENV GENOMIC AC012068 (2138) TAAAAAGAGCTGTACTTTGAACAATT-----

ENV GENOMIC AF277315 (2152) TATCTCTACTTAA-----

ENV GENOMIC AF027650 (700) -----

ENV GENOMIC AC078899 (2405) TTTCTCTACTTAAAGAGAAATTCCTCTGCCTTGAGATGCTGTAA-----

ENV GENOMIC HERV-KII (1850) TTTCTCTACTTAA-----

ENV GENOMIC AC008813 (1238) -----

ENV GENOMIC AC012309 (2133) TTTCTCTACTTAA-----

ENV GENOMIC AL121932 (1538) -----

ENV GENOMIC AD000090 (2157) TTTCTCTACTTAA-----

ENV GEN AL160008 (647) -----

ENV GENOMIC HEU32496 (441) -----

ENV GENOMIC AC011467 (1699) -----

ENV GENOMIC AF235103 (2212) TAAAAAGAGCTGTACTTTGAACAATTGCTTGTCTCAGATGTTGTTAATTGTAGTTTT-----

ENV GENOMIC AC026786 (2086) TAAAAAGAGCTGTACTTTAAACAATTGCTTGTCTGAGATGTTGTTAATTGTAGCTTCCCCAGCC-----

ENV GENOMIC AC034203 (1403) -----

ENV GENOMIC AC018809 (1846) TTTCTCTACTTAA-----

ENV GENOMIC HERV-KI02 AF164610 (1906) TTTTACTTACTTAAAGAAAAATTCCT-----

ENV GENOMIC FRAG. AF260253 (385) TTTCTCTACTTAA-----

CONSENSUS (2641) TG TGTAC

## FIGURE 7

1 60

GI\_4185938\_EMB\_CAA76878.1 (1) ----MGQTKSKIISKYASYLSFIKILLKRGGVVKVSTKNLIKLFQIIEQFCPWFPBQGTIL

GI\_4185942\_EMB\_CAA76881.1 (1) ----MGQTKSKIISKYASYLSFIKILLKRGGVVKVSTKNLIKLFQIIEQFCPWFPBQGTIL

GI\_4185946\_EMB\_CAA76884.1 (1) ----MGQTKSKIISKYASYLSFIKILLKRGGVVKVSTKNLIKLFQIIEQFCPWFPBQGTIL

GI\_5931704\_EMB\_CAB56602.1 (1) ----MGQTKTKSKYASYLSFIKILLKRGGVVKVSTKNLIKLFQIIEQFCPWFPBQGTIL

GAG OF AB047240 (1) ----MGQTKSKTKSKYASYLSFIKILLKRGGVVKVSTKNLIKLFQIIEQFCPWFPBQGTIL

TRANSLATION OF ORF99 (1) YKKAGLGQTKSKTKSKYASYLSFIKILLKRGGVVKVSTKNLIKLFQIIEQFCPWFPBQGTIL

TRANSLATION OF G226TOP-LINK (1) ----

TRANSLATION OF G591TOP-LINK (1) ----

TRANSLATION OF LNCAP-GAG (1) ----MGQTKSKTKSKYASYLSFIKILLKRGGVVKVSTKNLIKLFQIIEQFCPWFPBQGTIL

GAG106-135 (1) ----

GAG186-215 (1) ----

GAG46-75 (1) ----CPWFPEQGTIL

PDG-G1 (1) ----

PGD-G2 (1) ----

PGD-G3 (1) ----

CONSENSUS (1) CPWFPEQG L

61 120

GI\_4185938\_EMB\_CAA76878.1 (56) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

GI\_4185942\_EMB\_CAA76881.1 (56) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

GI\_4185946\_EMB\_CAA76884.1 (56) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

GI\_5931704\_EMB\_CAB56602.1 (54) DLEDWKRIKELKQAGRKGNIPLTVWNDWPIKAALEPPQTEDSVSVSDAPGSCI IDC

GAG OF AB047240 (56) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

TRANSLATION OF ORF99 (61) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

TRANSLATION OF G226TOP-LINK (1) ----

TRANSLATION OF G591TOP-LINK (1) ----

TRANSLATION OF LNCAP-GAG (56) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

GAG106-135 (1) ----DAPGSCI IDC

GAG186-215 (1) ----

GAG46-75 (11) DLKDWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

PDG-G1 (1) ----DWKRIKELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

PGD-G2 (1) ----

PGD-G3 (1) ----

CONSENSUS (61) DL DWKRIG ELKQAGRKGNIPLTVWNDWAIKAALEPPQTEDSVSVSDAPGSCI IDC

## FIGURE 7 CONTD...

GI_4185938_EMB_CAA76884.1_	(116)	NENTRKKKSQKETEGHLHCEYVVAEPVMAQSTQNVDYNQLQEVIIYPETLKLEGKGPPELVGPSE	121	180
GI_4185942_EMB_CAA76881.1_	(116)	NENTRKKKSQKETESLHCEYVVAEPVMAQSTQNVDYNQLQEVIIYPETLKLEGKGPPELVGPSE		
GI_4185946_EMB_CAA76884.1_	(116)	NENTRKKKSQKETEGHLHCEYVVAEPVMAQSTQNVDYNQLQEVIIYPETLKLEGKGPPELVGPSE		
GI_5931704_EMB_CAB56602.1_	(113)	NEKTRKKKSQKETETLHCEYVVAEPVMAQSTQNVDYNQLQEVIIYPETLKLEGKGPPELVGPSE		
GAG OF AB047240	(116)	NEKTGRKKKSQKETESLHCEYVTEPVMMAQSTQNVDYNQLQGVIIYPETLKLEGKGPPELVGPSE		
TRANSLATION OF ORF99	(121)	NEKTGRKKKSQKETESLHCEYVTEPVMMAQSTQNVDYNQLQGVIIYPETLKLEGKGPPELVGPSE		
TRANSLATION OF G226TOP-LINK	(1)	-----		
TRANSLATION OF G591TOP-LINK	(1)	-----		
TRANSLATION OF LNCAP-GAG	(116)	NEKTGRKKKSQKETESLHCEYVTEPVMMAQSTQNVDYNQLQGVIIYPETLKLEGKGPPELVGPSE		
GAG106-135	(11)	NENTRKKKSQKETEGHLHCEYV-----		
GAG186-215	(1)	-----		
GAG46-75	(31)	-----		
PDG-G1	(17)	-----		
PGD-G2	(1)	-----		
PGD-G3	(1)	-----		
CONSENSUS	(121)	NE T KKSQKETE LHCEYV		
GI_4185938_EMB_CAA76884.1_	(176)	SKPRGTSPLPAGQVPVTLQPQKQV-----	181	240
GI_4185942_EMB_CAA76881.1_	(176)	SKPRGTSRLPAGQVPVTLQPQKQV-----		
GI_4185946_EMB_CAA76884.1_	(176)	SKPRGTSPLPAGQVPVTLQPQKQV-----		
GI_5931704_EMB_CAB56602.1_	(173)	SKPRGSPSLPAGQVTVTLQPQAQV-----		
GAG OF AB047240	(176)	SKPRGSPSLPAGQVPVTLQPQKQV-----		
TRANSLATION OF ORF99	(181)	SKPRGSPSLPAGQVPVTLQPQKQV-----		
TRANSLATION OF G226TOP-LINK	(1)	-----		
TRANSLATION OF G591TOP-LINK	(1)	-----		
TRANSLATION OF LNCAP-GAG	(176)	SKPRGSPSLPAGQVPVTLQPQKQV-----		
GAG106-135	(31)	-----		
GAG186-215	(1)	-----AGQVPVTLQPQKQV-----		
GAG46-75	(31)	-----		
PDG-G1	(17)	-----		
PGD-G2	(1)	-----		
PGD-G3	(1)	-----		
CONSENSUS	(181)	AGQV VTLQPQ QVKENKTQ PVAYQYWPP SQYGY GMPP		
GI_4185938_EMB_CAA76884.1_	(236)	APQGRAPYPQPPTTRLNPTAPPSRQGSKLHEIIDKSRKEGDTAWQFPVTLQVQAGEET	241	300
GI_4185942_EMB_CAA76881.1_	(236)	APQGRAPYPQPPTTRLNPTAPPSRQGSKLHEIIDKSRKEGDTAWQFPVTLQVQAGEET		
GI_4185946_EMB_CAA76884.1_	(236)	APQGRAPYPQPPTTRLNPTAPPSRQGSKLHEIIDKSRKEGDTAWQFPVTLQVQAGEET		
GI_5931704_EMB_CAB56602.1_	(233)	APQDREPYPQPPTTRRQCYGTT-----		
GAG OF AB047240	(236)	ALQGRAPYPQPPTVRLNPTASRSQGGTTLHAVIDEARKQGDLEAWRFLVILQLVQAGEET		
TRANSLATION OF ORF99	(241)	ALQGRAPYPQPPTVRLNPTASRSQGGTTLHAVIDEARKQGDLEAWRFLVILQLVQAGEET		
TRANSLATION OF G226TOP-LINK	(11)	APQGRAPYPQPPTTRLNPTA-----		
TRANSLATION OF G591TOP-LINK	(1)	-----		
TRANSLATION OF LNCAP-GAG	(236)	ALQGRAPYPQPPTVRLNPTASRSQGGTTLHAVIDEARKQGDLEAWRFLVILQLVQAGEET		
GAG106-135	(31)	-----		
GAG186-215	(31)	-----		
GAG46-75	(31)	-----		
PDG-G1	(17)	-----		
PGD-G2	(1)	-----SKLHEIIDKSRKEGDT-----		
PGD-G3	(1)	-----		
CONSENSUS	(241)	A Q R PYPQPPT R		
GI_4185938_EMB_CAA76884.1_	(296)	QEGEPPTVEARYKSFSIKKLDKMDKEGVKQYGNPSYMRLLDSIAHGHRLLIPYDWESLAK	301	360
GI_4185942_EMB_CAA76881.1_	(296)	QEGEPPTVEARYKSFSIKKLDKMDKEGVKQYGNPSYMRLLDSIAHGHRLLIPYDWESLAK		
GI_4185946_EMB_CAA76884.1_	(296)	QEGEPPTVEARYKSFSIKKLDKMDKEGVKQYGNPSYMRLLDSIAHGHRLLIPYDWESLAK		
GI_5931704_EMB_CAB56602.1_	(254)	-----		
GAG OF AB047240	(296)	QVGAPARAETRCPEFTMKMLKDIKEGVKQYGSNSPYIRLLDSIAHGHRLLTPYDWESLAK		
TRANSLATION OF ORF99	(301)	QVGAPARAETRCPEFTMKMLKDIKEGVKQYGSNSPYIRLLDSIAHGHRLLTPYDWESLAK		
TRANSLATION OF G226TOP-LINK	(31)	-----		
TRANSLATION OF G591TOP-LINK	(1)	-----		
TRANSLATION OF LNCAP-GAG	(296)	QVGAPARAETRCPEFTMKMLKDIKEGVKQYGSNSPYIRLLDSIAHGHRLLTPYDWESLAK		
GAG106-135	(31)	-----		
GAG186-215	(31)	-----		
GAG46-75	(31)	-----		
PDG-G1	(17)	-----		
PGD-G2	(17)	-----		
PGD-G3	(1)	-----		
CONSENSUS	(301)			

## FIGURE 7 CONTD...

		361	420
GI_4185938_EMB_CAA76878.1	(356)	SSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPVNIDADQLLGIGQNWSTISQQALMQNEA	
GI_4185942_EMB_CAA76881.1	(356)	SSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPVNIDADQLLGIGQNWSTISQQALMQNEA	
GI_4185946_EMB_CAA76884.1	(356)	SSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPVNIDADQLLGIGQNWSTISQQALMQNEA	
GI_5931704_EMB_CAB56602.1	(254)	-----	
GAG OF AB047240	(356)	SSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA	
TRANSLATION OF ORF99	(361)	SSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA	
TRANSLATION OF G226TOP-LINK	(31)	-----	
TRANSLATION OF G591TOP-LINK	(1)	-----	
TRANSLATION OF LNCAP-GAG	(356)	SSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA	
GAG106-135	(31)	-----	
GAG186-215	(31)	-----	
GAG46-75	(31)	-----	
PDG-G1	(17)	-----	
PDG-G2	(17)	-----	
PDG-G3	(1)	-----	
CONSENSUS	(361)	-----	
		421	480
GI_4185938_EMB_CAA76878.1	(416)	IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVI	
GI_4185942_EMB_CAA76881.1	(416)	IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVI	
GI_4185946_EMB_CAA76884.1	(416)	IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVI	
GI_5931704_EMB_CAB56602.1	(254)	-----	
GAG OF AB047240	(416)	IEQVRAICLRAWGKIQDPGTAPP-INSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI	
TRANSLATION OF ORF99	(421)	IEQVRAICLRAWGKIQDPGTAPP-PINSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI	
TRANSLATION OF G226TOP-LINK	(31)	-----	
TRANSLATION OF G591TOP-LINK	(1)	-----	
TRANSLATION OF LNCAP-GAG	(416)	IEQVRAICLRAWGKIQDPGTAPP-INSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI	
GAG106-135	(31)	-----	
GAG186-215	(31)	-----	
GAG46-75	(31)	-----	
PDG-G1	(17)	-----	
PDG-G2	(17)	-----	
PDG-G3	(1)	-----	
CONSENSUS	(421)	-----	
		481	540
GI_4185938_EMB_CAA76878.1	(476)	VELMAYENANPECQSAIKPLKGKVPAGSDVISEYVKACDGIIGGAMYKAMLMAQAITGVVL	
GI_4185942_EMB_CAA76881.1	(476)	VELMAYENANPECQSAIKPLKGKVPAGSDVISEYVKACDGMGGAMHKAMLMAQAITGVVL	
GI_4185946_EMB_CAA76884.1	(476)	VELMAYENANPECQSAIKPLKGKVPAGSDVISEYVKACDGIIGGAMHKAMLMAQAITGVVL	
GI_5931704_EMB_CAB56602.1	(254)	-----	
GAG OF AB047240	(475)	VELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIIGGAMHKAMLMAQAMRGLTL	
TRANSLATION OF ORF99	(480)	VELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIIGGAMHKAMLMAQAMRGLTL	
TRANSLATION OF G226TOP-LINK	(31)	-----	
TRANSLATION OF G591TOP-LINK	(1)	-----	
TRANSLATION OF LNCAP-GAG	(475)	VELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIIGGAMHKAMLMAQAMRGLTL	
GAG106-135	(31)	-----	
GAG186-215	(31)	-----	
GAG46-75	(31)	-----	
PDG-G1	(17)	-----	
PDG-G2	(17)	-----	
PDG-G3	(1)	-----	
CONSENSUS	(481)	-----	
		541	600
GI_4185938_EMB_CAA76878.1	(536)	GGQVRTFGRKCYNCQGIHGLKKNCPLVNLKQNIITQATTG-REPPDLCPRCCKGKHWSQ	
GI_4185942_EMB_CAA76881.1	(536)	GGQVRTFGRKCYNCQGIHGLKKNCPLVNLKQNIITQATTG-REPPDLCPRCCKGKHWSQ	
GI_4185946_EMB_CAA76884.1	(536)	GGQVRTFGRKCYNCQGIHGLKKNCPLVNLKQNIITQATTG-REPPDLCPRCCKGKHWSQ	
GI_5931704_EMB_CAB56602.1	(254)	-----	
GAG OF AB047240	(535)	GGQVRTFGRKCYNCQGIHGLKRSCLVNLKQNIINQAITAKNKKPSGLCPKCGKGKHWSQ	
TRANSLATION OF ORF99	(540)	GGQVRTFGRKCYNCQGIHGLKRSCLVNLKQNIINQAITAKNKKPSGLCPKCGKGKHWSQ	
TRANSLATION OF G226TOP-LINK	(31)	-----	
TRANSLATION OF G591TOP-LINK	(1)	-----	
TRANSLATION OF LNCAP-GAG	(535)	GGQVRTFGRKCYNCQGIHGLKRSCLVNLKQNIINQAITAKNKKPSGLCPKCGKGKHWSQ	
GAG106-135	(31)	-----	
GAG186-215	(31)	-----	
GAG46-75	(31)	-----	
PDG-G1	(17)	-----	
PDG-G2	(17)	-----	
PDG-G3	(1)	-----	
CONSENSUS	(541)	-----	

**FIGURE 7 CONTD...**

		601		660
GI_4185938	EMB_CAA76878.1	(595)	CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFFIQPFVFPQGFGQQQP-PLSQVFQGISQLPQ	
GI_4185942	EMB_CAA76881.1	(595)	CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFFIQPFVPHGFGQQQP-PLSQVFQGISQLPQ	
GI_4185946	EMB_CAA76884.1	(595)	CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFFIQPFVFPQGFGQQQP-PLSQVFQGISQLPQ	
GI_5931704	EMB_CAB56602.1	(254)	-----	
	GAG OF AB047240	(595)	CHSKFDKDGQPLSGNRRKGQPQAPQQTGAFFVQLVFPVPGFGQQQPLQKIPPLQGVSQLQQ	
	TRANSLATION OF ORF99	(600)	CHSKFDKDGQPLSGNRRKGQPQAPQQTGAFFVQLVFPVPGFGQQQPLQKIPPLQGVSQLQQ	
	TRANSLATION OF G226TOP-LINK	(31)	-----	
	TRANSLATION OF G591TOP-LINK	(5)	CRSKFDKNGQPLSGNEQRGQPQAPQ	
	TRANSLATION OF LNCAP-GAG	(595)	CHSKFDKDGQPLSGNRRKGQPQAPQQTGAFFVQLVFPVPGFGQQQPLQKIPPLQGVSQLQQ	
	GAG106-135	(31)	-----	
	GAG186-215	(31)	-----	
	GAG46-75	(31)	-----	
	PGD-G1	(17)	-----	
	PGD-G2	(17)	-----	
	PGD-G3	(1)	CRSKFDKNGQPLSGNE-----	
	CONSENSUS	(601)	C SKFDK GQPLSGN	

		661	673
GI_4185938	EMB_CAA76878.1	(654)	YNNCPPPPQAAVQQ
GI_4185942	EMB_CAA76881.1	(654)	YNNCPPPPQAAVQQ
GI_4185946	EMB_CAA76884.1	(654)	YNNCPPPPQAAVQQ
GI_5931704	EMB_CAB56602.1	(254)	
	GAG OF AB047240	(655)	SNSCPAPQQAAPQ
	TRANSLATION OF ORF99	(660)	SNSCPAPQQAAPQ
	TRANSLATION OF G226TOP-LINK	(31)	-----
	TRANSLATION OF G591TOP-LINK	(31)	-----
	TRANSLATION OF LNCAP-GAG	(655)	SNSCPAPQQAAPQ
	GAG106-135	(31)	-----
	GAG186-215	(31)	-----
	GAG46-75	(31)	-----
	PDG-G1	(17)	-----
	PDG-G2	(17)	-----
	PDG-G3	(17)	-----
	CONSENSUS	(661)	

**FIGURE 8**

		1		120
GI_4185939_EMB_CAA76879.1	(1)	MLTDLRAVN---AVIQPMGLPQGLPSPAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFA		
GI_4185943_EMB_CAA76882.1	(1)	MLTDLRAVNNAVNAVIQPMGLPQGLPSLAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFA		
GI_4185947_EMB_CAA76885.1	(1)	MLTDLRAVN---AVIQPMGLPQGLPSPAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFA		
GI_5931705_EMB_CAB56603.1	(1)	-----MIPKDWPLIIIDLKDCFFTIPLAEQDCEKFA		
ENV OF AB047240	(1)	-----		
TRANSLATION OF P386TOP-LINK	(1)	-----		
TRANSLATION OF POL349-LINK	(1)	-----		
LNCAP-GENOMEA-POLORF	(1)	-----		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	-----		
TRANSLATION OF ORF111-10	(1)	-----		
PGD-P1	(1)	-----		
PGD-P2	(1)	-----		
PGDP3	(1)	-----		
CONSENSUS	(1)	-----		
		61		120
GI_4185939_EMB_CAA76879.1	(58)	FTTIPAINNKEPATRFQWKVLPQGMNLSPTICQTFFVGRALQPVREKFSDCYIIHCIDDILC		
GI_4185943_EMB_CAA76882.1	(61)	FTTIPAINNKEPATRFQWKVLPQGMNLSPTICQTFFVGRALQPVREKFSDCYIIHYIDDILC		
GI_4185947_EMB_CAA76885.1	(58)	FTTIPAINNKEPATRFQWKVLPQGMNLSPTICQTFFVGRALQPVREKFSDCYIIHCIDDILC		
GI_5931705_EMB_CAB56603.1	(32)	FTTIPAINNKEPATRFQWKVLPQGMNLSPTLCQTFFVGRALQPVRRKFSDCYIIHYFDDILC		
ENV OF AB047240	(1)	-----		
TRANSLATION OF P386TOP-LINK	(1)	-----		
TRANSLATION OF POL349-LINK	(1)	-----		
LNCAP-GENOMEA-POLORF	(1)	-----		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	-----		
TRANSLATION OF ORF111-10	(1)	-----		
PGD-P1	(1)	-----		
PGD-P2	(1)	-----		
PGDP3	(1)	-----		
CONSENSUS	(61)	-----		

## FIGURE 8 CONTD...

GI_4185939_EMB_CAA76879.1	(118)	AAETKDKLIDCYTFLQAEVANAGLAIASDKIQSTSPFFHYLGMQIENRKIKPKQKIEIRKDT	121		180
GI_4185943_EMB_CAA76882.1	(121)	AAEMKDKLIDCYTFLQAEVANAGLAIASDKIQSTSPFFHYLEMQIENRKIKPKKIEIRKDT	(121)		
GI_4185947_EMB_CAA76885.1	(118)	AAETKDKLIDCYTFLQAEVANAGLAIASDKIQSTSPFFHYLGMQIENRKIKPKQKIEIRKDT	(118)		
GI_5931705_EMB_CAB56603.1	(92)	AAETKDKLIDCYTFLQAEVANAGLAIASDKIQSTSPFFHYLGMQIENRKIKPKKIEIRKDT	(92)		
ENV OF AB047240	(1)	-----	(1)		
TRANSLATION OF P386TOP-LINK	(1)	-----	(1)		
TRANSLATION OF POL349-LINK	(1)	-----	(1)		
LNCAP-GENOMEA-POLORF	(1)	-----	(1)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	-----	(1)		
TRANSLATION OF ORF111-10	(1)	-----	(1)		
PGD-P1	(1)	-----	(1)		
PGD-P2	(1)	-----	(1)		
PGDP3	(1)	-----	(1)		
CONSENSUS	(121)	-----	(121)		
GI_4185939_EMB_CAA76879.1	(178)	LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGSDLSNKRMLTPEATKEIKLVEE	181		240
GI_4185943_EMB_CAA76882.1	(181)	LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGSDLSNKRMLTPEATKEIKLVEE	(181)		
GI_4185947_EMB_CAA76885.1	(178)	LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGSDLSNKRMLTPEATKEIKLVEE	(178)		
GI_5931705_EMB_CAB56603.1	(152)	LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGSDLSNKRMLTPEATKEIKLVEE	(152)		
ENV OF AB047240	(1)	-----	(1)		
TRANSLATION OF P386TOP-LINK	(1)	-----	(1)		
TRANSLATION OF POL349-LINK	(1)	-----	(1)		
LNCAP-GENOMEA-POLORF	(1)	-----	(1)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	-----	(1)		
TRANSLATION OF ORF111-10	(1)	-----	(1)		
PGD-P1	(17)	-----	(17)		
PGD-P2	(1)	-----	(1)		
PGDP3	(1)	-----	(1)		
CONSENSUS	(181)	-----	(181)		
GI_4185939_EMB_CAA76879.1	(238)	KIQSAQINRIDPLAPQLLIFATAHSPTIIQNTDLVWSFLPHSTTKTFTLYLDQMAT	241		300
GI_4185943_EMB_CAA76882.1	(241)	KIQSAQINRIDPLAPQLLIFATAHSPTIIQNTDLVWSFLPHSTTKTFTLYLDQMAT	(241)		
GI_4185947_EMB_CAA76885.1	(238)	KIQSAQINRIDPLAPQLLIFATAHSPTIIQNTDLVWSFLPHSTTKTFTLYLDQMAT	(238)		
GI_5931705_EMB_CAB56603.1	(212)	KIQSAQINRIDPLAPQLLIFATAHSPTIIQNTDLVWSFLPHSTTKTFTLYLDQMAT	(212)		
ENV OF AB047240	(1)	-----	(1)		
TRANSLATION OF P386TOP-LINK	(1)	-----	(1)		
TRANSLATION OF POL349-LINK	(1)	-----	(1)		
LNCAP-GENOMEA-POLORF	(1)	-----	(1)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(1)	-----	(1)		
TRANSLATION OF ORF111-10	(1)	-----	(1)		
PGD-P1	(17)	-----	(17)		
PGD-P2	(1)	-----	(1)		
PGDP3	(1)	-----	(1)		
CONSENSUS	(241)	D LAPLQLLIFATAHS TGIIQNTDLVWSFLPHSTVKTFTLYLDQMAT	(241)		
GI_4185939_EMB_CAA76879.1	(298)	LIGQRLRIIILCGNDPDKIVVPLTKEQVROAFINSQAWQIGLANFGLIDNHYPKTKIF	301		360
GI_4185943_EMB_CAA76882.1	(301)	LIGQRLRIIILCGNDPDKIVVPLTKEQVROAFINSQAWQIGLANFGLIDNHYPKTKIF	(301)		
GI_4185947_EMB_CAA76885.1	(298)	LIGQRLRIIILCGNDPDKIVVPLTKEQVROAFINSQAWQIGLANFGLIDNHYPKTKIF	(298)		
GI_5931705_EMB_CAB56603.1	(272)	LIGQRLRIIILCGNDPDKIVVPLTKEQVROAFINSQAWQIGLANFGLIDNHYPKTKIF	(272)		
ENV OF AB047240	(4)	LIGQRLRIIILCGNDPDKITVPFNKQVROAFISSQAWQIGLANFGLIDNHYPKTKIF	(4)		
TRANSLATION OF P386TOP-LINK	(1)	-----	(1)		
TRANSLATION OF POL349-LINK	(1)	-----	(1)		
LNCAP-GENOMEA-POLORF	(51)	LIGQRLRIIILCGNDPDKITVPFNKQVROAFISSQAWQIGLANFGLIDNHYPKTKIF	(51)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(51)	LIGQRLRIIILCGNDPDKITVPFNKQVROAFISSQAWQIGLANFGLIDNHYPKTKIF	(51)		
TRANSLATION OF ORF111-10	(57)	LIGQRLRIIILCGNDPDKITVPFNKQVROAFISSQAWQIGLANFGLIDNHYPKTKIF	(57)		
PGD-P1	(17)	-----	(17)		
PGD-P2	(1)	-----	(1)		
PGDP3	(1)	-----	(1)		
CONSENSUS	(301)	LIGQ RLRII LCGNDPDKI VP K QVRQAFI SGAW IGLANFGLIDNHYPKTKIF	(301)		
GI_4185939_EMB_CAA76879.1	(358)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAATGPKERVIKTPYQSAQRAELVAV	361		420
GI_4185943_EMB_CAA76882.1	(361)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAATGPKERVIKTPYQSAQRAELVAV	(361)		
GI_4185947_EMB_CAA76885.1	(358)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAATGPKERVIKTPYQSAQRAELVAV	(358)		
GI_5931705_EMB_CAB56603.1	(332)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAATGPKERVIKTPYQSAQRAELVAV	(332)		
ENV OF AB047240	(64)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAATGPKERVIKTPYQSAQRAELVAV	(64)		
TRANSLATION OF P386TOP-LINK	(1)	-----	(1)		
TRANSLATION OF POL349-LINK	(10)	QFLKLTWILPKITRREP-----	(10)		
LNCAP-GENOMEA-POLORF	(111)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAATGPKERVIKTPYQSAQRAELVAV	(111)		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(111)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAATGPKERVIKTPYQSAQRAELVAV	(111)		
TRANSLATION OF ORF111-10	(117)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAATGPKERVIKTPYQSAQRAELVAV	(117)		
PGD-P1	(17)	-----	(17)		
PGD-P2	(1)	-----	(1)		
PGDP3	(1)	-----	(1)		
CONSENSUS	(361)	QFLKLTWILPKITRREPLENALTVFTDGSSNGKAAATGPKERVIKTPYQSAQRAELVAV	(361)		



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**FIGURE 8 contd...**

GI_4185939_EMB_CAA76879.1	(418)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDQNLNQLFNLLQQTVRKRNFPFYI	421	480
GI_4185943_EMB_CAA76882.1	(421)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDQNLNQLFNLLQQTVRKRNFPFYI		
GI_4185947_EMB_CAA76885.1	(418)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDQNLNQLFNLLQQTVRKRNFPFYI		
GI_5931705_EMB_CAB56603.1	(392)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDQNLNQLFNLLQQTVRKRNFPFYI		
ENV OF AB047240	(124)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFPFYI		
TRANSLATION OF P386TOP-LINK	(31)	-----		
TRANSLATION OF POL349-LINK	(28)	-----		
LNCAP-GENOMEA-POLORF	(171)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFPFYI		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(171)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFPFYI		
TRANSLATION OF ORF111-10	(177)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFPFYI		
PGD-P1	(17)	-----		
PGD-P2	(17)	-----		
PGDP3	(1)	-----		
CONSENSUS	(421)	ITVLQDFDQPINIISDSAYVVQATRDVETALIKYS DD LNQLFNLLQQTVRKRNFPFYI		
GI_4185939_EMB_CAA76879.1	(478)	THIRAHNTLPGPLTKANEQADLLVSSALIKAEQLHALTHVNAAGLKNKFDVTWKQAKDIV	481	540
GI_4185943_EMB_CAA76882.1	(481)	THIRAHNTLPGPLTKANEQADLLVSSALIKAEQLHALTHVNAAGLKNKFDVTWKQAKDIV		
GI_4185947_EMB_CAA76885.1	(478)	THIRAHNTLPGPLTKANEQADLLVSSALIKAEQLHALTHVNAAGLKNKFDVTWKQAKDIV		
GI_5931705_EMB_CAB56603.1	(452)	THIRAHNTLPGPLTKANEQADLLVSSAFIKAEQLHALTHVNAAGLKNKFDVTWKQAKDIV		
ENV OF AB047240	(184)	THIRAHNTLPGPLTKANEQADLLVSSAFIKAEQLLALTHVNAAGLKNKFDVTWKQAKDIV		
TRANSLATION OF P386TOP-LINK	(31)	-----		
TRANSLATION OF POL349-LINK	(28)	-----		
LNCAP-GENOMEA-POLORF	(231)	THIRAHNTLPGPLTKANEQADLLVSSAFIKAEQLLALTHVNAAGLKNKFDVTWKQAKDIV		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(231)	THIRAHNTLPGPLTKANEQADLLVSSAFIKAEQLLALTHVNAAGLKNKFDVTWKQAKDIV		
TRANSLATION OF ORF111-10	(237)	THIRAHNTLPGPLTKANEQADLLVSSAFIKAEQLLALTHVNAAGLKNKFDVTWKQAKDIV		
PGD-P1	(17)	-----		
PGD-P2	(17)	-----		
PGDP3	(1)	-----		
CONSENSUS	(481)	THIRAHNTLPGPLTKANEQADLLVSSA IKAQL ALTHVNAAGLKNKFDVTWKQAKDIV		
GI_4185939_EMB_CAA76879.1	(538)	QHCTQCQVLHLPTQEBAGVNPRLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIMATC	541	600
GI_4185943_EMB_CAA76882.1	(541)	QHCTQCQVLHLPTQEBAGVNPRLCPNALWQMDVTHVSSFGRLSYVHVTVDTYSHFIMATC		
GI_4185947_EMB_CAA76885.1	(538)	QHCTQCQVLHLPTQEBAGVNPRLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIMATC		
GI_5931705_EMB_CAB56603.1	(512)	QHCTQCQVLHLPTQEBAGVNPRLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIMATC		
ENV OF AB047240	(244)	QHCTQCQVLHLPTQEBAGVNPRLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIMATC		
TRANSLATION OF P386TOP-LINK	(31)	-----		
TRANSLATION OF POL349-LINK	(28)	-----		
LNCAP-GENOMEA-POLORF	(291)	QHCTQCQVLHLPTQEBAGVNPRLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIMATC		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(291)	QHCTQCQVLHLPTQEBAGVNPRLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIMATC		
TRANSLATION OF ORF111-10	(297)	QHCTQCQVLHLPTQEBAGVNPRLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIMATC		
PGD-P1	(17)	-----		
PGD-P2	(17)	-----		
PGDP3	(1)	-----		
CONSENSUS	(541)	QHCTQCQVLHL PTQEBAGVNPRLCPNALWQMD THV SPGRLSYVHVTVDTYSHFIMATC		
GI_4185939_EMB_CAA76879.1	(598)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG	601	660
GI_4185943_EMB_CAA76882.1	(601)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
GI_4185947_EMB_CAA76885.1	(598)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
GI_5931705_EMB_CAB56603.1	(572)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
ENV OF AB047240	(304)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
TRANSLATION OF P386TOP-LINK	(31)	-----		
TRANSLATION OF POL349-LINK	(28)	-----		
LNCAP-GENOMEA-POLORF	(351)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(351)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
TRANSLATION OF ORF111-10	(357)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
PGD-P1	(17)	-----		
PGD-P2	(17)	-----		
PGDP3	(1)	-----		
CONSENSUS	(601)	QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPIYNSQG		
GI_4185939_EMB_CAA76879.1	(658)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT	661	720
GI_4185943_EMB_CAA76882.1	(661)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT		
GI_4185947_EMB_CAA76885.1	(658)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT		
GI_5931705_EMB_CAB56603.1	(632)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAE-HLT		
ENV OF AB047240	(364)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT		
TRANSLATION OF P386TOP-LINK	(31)	-----		
TRANSLATION OF POL349-LINK	(28)	-----		
LNCAP-GENOMEA-POLORF	(411)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT		
TRANSLATION OF LNCAP-POL-GENA-GOODA	(411)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT		
TRANSLATION OF ORF111-10	(417)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT		
PGD-P1	(17)	-----		
PGD-P2	(17)	-----		
PGDP3	(1)	-----		
CONSENSUS	(661)	QAIVERTNRTLKTQLVKQKGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSA QHLT		

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## FIGURE 8 CONTD...

GI_4185939_EMB_CAA76879.1	(718)	GKKNSPHEGKLIWWKDSKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRLHKFYNEPI	721	780
GI_4185943_EMB_CAA76882.1	(721)	GKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRLHKFYNEPI	(721)	
GI_4185947_EMB_CAA76885.1	(718)	GKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRLHKFYNEPI	(718)	
GI_5931705_EMB_CAB56603.1	(691)	GKKNSPHEGKLI-----	(691)	
ENV OF AB047240	(424)	GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRLHKFYNEPI	(424)	
TRANSLATION OF P386TOP-LINK	(31)	-----	(31)	
TRANSLATION OF POL349-LINK	(28)	-----	(28)	
LNCAP-GENOMEA-POLORF	(471)	GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRLHKFYNEPI	(471)	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(471)	GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRLHKFYNEPI	(471)	
TRANSLATION OF ORF111-10	(477)	GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRLHKFYNEPI	(477)	
PGD-P1	(17)	-----	(17)	
PGD-P2	(17)	-----	(17)	
PGDP3	(4)	GKKNSPHEGKLI-----	(4)	
CONSENSUS	(721)	GKK SPHEGKLIWWKD KNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRLHKFYNEPI	(721)	
GI_4185939_EMB_CAA76879.1	(778)	RDAAKSTSAETETS-----	781	840
GI_4185943_EMB_CAA76882.1	(781)	GDAKKSTSAETETP-----	(781)	
GI_4185947_EMB_CAA76885.1	(778)	RDAAKSTSAETETS-----	(778)	
GI_5931705_EMB_CAB56603.1	(703)	-----	(703)	
ENV OF AB047240	(484)	GDAKKRASTEMVTPVTWMDNPIEVYVNDVSVWVPGFTDDRCAPKPEEEGMMINISIVYRYP	(484)	
TRANSLATION OF P386TOP-LINK	(31)	-----	(31)	
TRANSLATION OF POL349-LINK	(28)	-----	(28)	
LNCAP-GENOMEA-POLORF	(531)	GDAKKRASTEMVTPVTWMDNPIEVYVNDVSVWVPGFTDDRCAPKPEEEGMMINISIVYRYP	(531)	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(531)	GDAKKRASTEMVTPVTWMDNPIEVYVNDVSVWVPGFTDDRCAPKPEEEGMMINISIVYRYP	(531)	
TRANSLATION OF ORF111-10	(537)	GDAKKRASTEMVTPVTWMDNPIEVYVNDVSVWVPGFTDDRCAPKPEEEGMMINISIVYRYP	(537)	
PGD-P1	(17)	-----	(17)	
PGD-P2	(17)	-----	(17)	
PGDP3	(17)	-----	(17)	
CONSENSUS	(781)	DARK S E T	(781)	
GI_4185939_EMB_CAA76879.1	(792)	-----	841	900
GI_4185943_EMB_CAA76882.1	(795)	-----	(795)	
GI_4185947_EMB_CAA76885.1	(792)	-----	(792)	
GI_5931705_EMB_CAB56603.1	(703)	-----	(703)	
ENV OF AB047240	(544)	PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHVMVSGMSLRPRVNYLQDFSQYRSLKFR	(544)	
TRANSLATION OF P386TOP-LINK	(31)	-----	(31)	
TRANSLATION OF POL349-LINK	(28)	-----	(28)	
LNCAP-GENOMEA-POLORF	(591)	PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHVMVSGMSLRPRVNYLQDFSQYRSLKFR	(591)	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(591)	PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHVMVSGMSLRPRVNYLQDFSQYRSLKFR	(591)	
TRANSLATION OF ORF111-10	(597)	PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHVMVSGMSLRPRVNYLQDFSQYRSLKFR	(597)	
PGD-P1	(17)	-----	(17)	
PGD-P2	(17)	-----	(17)	
PGDP3	(17)	-----	(17)	
CONSENSUS	(841)	-----	(841)	
GI_4185939_EMB_CAA76879.1	(792)	-----	901	960
GI_4185943_EMB_CAA76882.1	(795)	-----	(795)	
GI_4185947_EMB_CAA76885.1	(792)	-----	(792)	
GI_5931705_EMB_CAB56603.1	(703)	-----	(703)	
ENV OF AB047240	(604)	PKGKPCPKKEIPKESKNTVLVWEECVANSVILQNNFEGTIDWAPRGQFYHNCSGQTQS	(604)	
TRANSLATION OF P386TOP-LINK	(31)	-----	(31)	
TRANSLATION OF POL349-LINK	(28)	-----	(28)	
LNCAP-GENOMEA-POLORF	(651)	PKGKPCPKKEIPKESKNTVLVWEECVANSVILQNNFEGTIDWAPRGQFYHNCSGQTQS	(651)	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(651)	PKGKPCPKKEIPKESKNTVLVWEECVANSVILQNNFEGTIDWAPRGQFYHNCSGQTQS	(651)	
TRANSLATION OF ORF111-10	(657)	PKGKPCPKKEIPKESKNTVLVWEECVANSVILQNNFEGTIDWAPRGQFYHNCSGQTQS	(657)	
PGD-P1	(17)	-----	(17)	
PGD-P2	(17)	-----	(17)	
PGDP3	(17)	-----	(17)	
CONSENSUS	(901)	-----	(901)	
GI_4185939_EMB_CAA76879.1	(816)	QEGRAANLTTKADAVSYKISREHKGDTNPREACSGDDCINGGKSPYCRSSCS---	961	1020
GI_4185943_EMB_CAA76882.1	(819)	QESRAADLTTKADAVSYKISREHKGDTNPREACSGDDCINGGKSPYCRSSCS---	(819)	
GI_4185947_EMB_CAA76885.1	(816)	QEGRAANLTTKADAVSYKISREHKGDTNPREACSGDDCINGGKSPYCRSSCS---	(816)	
GI_5931705_EMB_CAB56603.1	(703)	-----	(703)	
ENV OF AB047240	(664)	CPSAQVSPAVDSLTESLDKHKHKKLQSFYPWENGEKGSTPRPEIISPVS GPEHPFLWR	(664)	
TRANSLATION OF P386TOP-LINK	(31)	-----	(31)	
TRANSLATION OF POL349-LINK	(28)	-----	(28)	
LNCAP-GENOMEA-POLORF	(711)	CPSAQVSPAVDSLTESLDKHKHKKLQSFYPWENGEKGSTPRPEIISPVS GPEHPFLWR	(711)	
TRANSLATION OF LNCAP-POL-GENA-GOODA	(711)	CPSAQVSPAVDSLTESLDKHKHKKLQSFYPWENGEKGSTPRPEIISPVS GPEHPFLWR	(711)	
TRANSLATION OF ORF111-10	(717)	CPSAQVSPAVDSLTESLDKHKHKKLQSFYPWENGEKGSTPRPEIISPVS GPEHPFLWR	(717)	
PGD-P1	(17)	-----	(17)	
PGD-P2	(17)	-----	(17)	
PGDP3	(17)	-----	(17)	
CONSENSUS	(961)	A D K P EWG I SP S	(961)	

**FIGURE 8 CONTD...**

	1021	1035
GI_4185939_EMB_CAA76879.1	(873)	-----
GI_4185943_EMB_CAA76882.1	(876)	-----
GI_4185947_EMB_CAA76885.1	(873)	-----
GI_5931705_EMB_CAB56603.1	(703)	-----
ENV OF AB047240	(724)	LWPDITLEFGLEIKL
TRANSLATION OF P386TOP-LINK	(31)	-----
TRANSLATION OF POL349-LINK	(28)	-----
LNCAP-GENOMEA-POLORF	(764)	-----
TRANSLATION OF LNCAP-POL-GENA-GOODA	(771)	LWPDITLEFGLEIKL
TRANSLATION OF ORF111-10	(777)	LWPDITLEFGLEIKL
PGD-P1	(17)	-----
PGD-P2	(17)	-----
PGDP3	(17)	-----
CONSENSUS	(1021)	

**FIGURE 9**

	1	60
GI_4185940_EMB_CAA76880.1	(1)	-----
GI_4185944_EMB_CAA76883.1	(1)	-----
GI_4185948_EMB_CAA76886.1	(1)	-----
GI_5931706_EMB_CAB56604.1	(1)	-----
ENV OF AB047240	(1)	MATLIGQGRLRIITLCGNDPDKITVPFNKQQVRQAFISSGAWQIGLANFLGIIDNHYPKT
TRANSLATION OF E207TOP-LINK	(1)	-----
TRANSLATION OF ENV287-LINK	(1)	-----
TRANSLATION OF T20.22A-23	(1)	-----
PGD-E1	(1)	-----
PGD-E2	(1)	-----
PGD-E3	(1)	-----
CONSENSUS	(1)	

	61	120
GI_4185940_EMB_CAA76880.1	(1)	-----
GI_4185944_EMB_CAA76883.1	(1)	-----
GI_4185948_EMB_CAA76886.1	(1)	-----
GI_5931706_EMB_CAB56604.1	(1)	-----
ENV OF AB047240	(61)	KIPQFLKLTWILPKITRREPLENALTVFDTGSSNGKAAAYTGPKERVIKTPYQSAQRAEL
TRANSLATION OF E207TOP-LINK	(1)	-----
TRANSLATION OF ENV287-LINK	(1)	-----
TRANSLATION OF T20.22A-23	(1)	-----
PGD-E1	(1)	-----
PGD-E2	(1)	-----
PGD-E3	(1)	-----
CONSENSUS	(61)	

	121	180
GI_4185940_EMB_CAA76880.1	(1)	-----
GI_4185944_EMB_CAA76883.1	(1)	-----
GI_4185948_EMB_CAA76886.1	(1)	-----
GI_5931706_EMB_CAB56604.1	(1)	-----
ENV OF AB047240	(121)	VAVITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNF
TRANSLATION OF E207TOP-LINK	(1)	-----
TRANSLATION OF ENV287-LINK	(1)	-----
TRANSLATION OF T20.22A-23	(1)	-----
PGD-E1	(1)	-----
PGD-E2	(1)	-----
PGD-E3	(1)	-----
CONSENSUS	(121)	

81 240

	421	480
GI_4185940_EMB_CAA76880.1	(35)	PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPE\$M\$LLAALMIVSMVVSLPMPAGAAAA
GI_4185944_EMB_CAA76883.1	(35)	PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPE\$M\$LLAALMIVSMVVSLPMPAGAAAA
GI_4185948_EMB_CAA76886.1	(35)	PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPE\$M\$LLAALMIVSMVVSLPMPAGAAAA
GI_5931706_EMB_CAB56604.1	(1)	-----
ENV OF AB047240	(421)	HLTGKXKSPH\$G\$KLIWWKDNKNKTWEIGKVI TWGRGFACVSP\$G\$ENQLP\$V\$VIPTRHLLKFYN
TRANSLATION OF E207TOP-LINK	(1)	-----
TRANSLATION OF ENV287-LINK	(1)	-----
TRANSLATION OF T20.22A-23	(40)	PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPE\$M\$LLAALMIVSMVVSLPMPAGAAAA
PGD-E1	(1)	-----
PGD-E2	(1)	-----
PGD-E3	(1)	-----
CONSENSUS	(421)	

## FIGURE 9 CONTD...

GI\_4185940\_EMB\_CAA76880.1\_ (95) NYTYWAYVFPFP-~~IT~~RAVTWMDNPTEVYVNDVSVWVPGPIDDRCPAKPPEEGMMINISIGY 540  
 GI\_4185944\_EMB\_CAA76883.1\_ (95) NYTYWAYVFPFP-~~IT~~RAVTWMDNPTEVYVNDVSVWVPGPTDDHCPAKPPEEGMMINISIGY  
 GI\_4185948\_EMB\_CAA76886.1\_ (95) NYTYWAYVFPFP-~~IT~~RAVTWMDNPTEVYVNDVSVWVPGPIDDRCPAKPPEEGMMINISIGY  
 GI\_5931706\_EMB\_CAB56604.1\_ (1) -----~~IT~~PTVTWMDNPTEVYVNDVSVWVPGPTDDHCPAKPPEEGMMINISIGY  
 ENV OF AB047240 (481) EPIGDAKKRASTE~~IT~~PTVTWMDNPTEVYVNDVSVWVPGPTDDHCPAKPPEEGMMINISIVY  
 TRANSLATION OF E207TOP-LINK (1) -----  
 TRANSLATION OF ENV287-LINK (1) -----  
 TRANSLATION OF T20.22A-23 (100) NYTYWAYVFPFP-~~IT~~RAVTWMDNPTEVYVNDVSVWVPGPIDDRCPAKPPEEGMMINISIGY  
 PGD-E1 (1) -----  
 PGD-E2 (1) -----  
 PGD-E3 (1) -----  
 CONSENSUS (481) LI VTWMDNP EVYVNDVSVWVPGP DD CPAKPPEEGMMINISI Y

GI\_4185940\_EMB\_CAA76880.1\_ (154) HYPPICLGRAPGCM~~IT~~PAVQNLVEVPTVSPICRFTYHVMVSGMSLRPRVNYLQDFSQYRSL 541  
 GI\_4185944\_EMB\_CAA76883.1\_ (154) RYPPICLGRAPGCM~~IT~~PAVQNLVEVPTVSPISRFTYHVMVSGMSLRPRVNYLQDFSQYRSL 600  
 GI\_4185948\_EMB\_CAA76886.1\_ (154) HYPPICLGRAPGCM~~IT~~PAVQNLVEVPTVSPICRFTYHVMVSGMSLRPRVNYLQDFSQYRSL  
 GI\_5931706\_EMB\_CAB56604.1\_ (48) HYPPICLGRAPGCM~~IT~~PAVQNLVEVPTVSPNSRFTYHVMVSGMSLRPRVNYLQDFSQYRSL  
 ENV OF AB047240 (541) RYPPICLGRAPGCM~~IT~~PAVQNLVEVPTVSPNSRFTYHVMVSGMSLRPRVNYLQDFSQYRSL  
 TRANSLATION OF E207TOP-LINK (1) -----FSYQYRSL  
 TRANSLATION OF ENV287-LINK (1) -----  
 TRANSLATION OF T20.22A-23 (159) HYPPICLGRAPGCM~~IT~~PAVQNLVEVPTVSPICRFTYHVMVSGMSLRPRVNYLQDFSQYRSL  
 PGD-E1 (1) -----  
 PGD-E2 (1) -----  
 PGD-E3 (1) -----  
 CONSENSUS (541) YPPICLGRAPGCM~~IT~~PAVQNLVEVPTVSP RFTYHVMVSGMSLRPRVN LQDFSQYRSL

GI\_4185940\_EMB\_CAA76880.1\_ (214) KFRPKGKPCPKKEIPKESKNT~~IT~~EVLVWEECVANS~~IT~~AVILQNN~~IT~~EFGTIIDWAPRGQFYHNCSSGQ 601  
 GI\_4185944\_EMB\_CAA76883.1\_ (214) KFRPKGKPCPKKEIPKESKNT~~IT~~EVLVWEECVANS~~IT~~AVILQNN~~IT~~EFGTIIDWAPRGQFYHNCSSGQ 660  
 GI\_4185948\_EMB\_CAA76886.1\_ (214) KFRPKGKPCPKKEIPKESKNT~~IT~~EVLVWEECVANS~~IT~~AVILQNN~~IT~~EFGTIIDWAPRGQFYHNCSSGQ  
 GI\_5931706\_EMB\_CAB56604.1\_ (108) KFRPKGKTCPKKEIPKESKNT~~IT~~EVLVWEECVANS~~IT~~VVILQNN~~IT~~EFGTIIDWAPRGQFYHNCSSGQ  
 ENV OF AB047240 (601) KFRPKGKPCPKKEIPKESKNT~~IT~~EVLVWEECVANS~~IT~~AVILQNN~~IT~~EFGTIIDWAPRGQFYHNCSSGQ  
 TRANSLATION OF E207TOP-LINK (8) KFRPKGKPCPKKEIPKESKNT~~IT~~EVLVWEECVANS~~IT~~AVILQNN~~IT~~EFGTIIDWAPRGQFYHNCSSGQ  
 TRANSLATION OF ENV287-LINK (1) -----  
 TRANSLATION OF T20.22A-23 (219) KFRPKGKPCPKKEIPKESKNT~~IT~~EVLVWEECVANS~~IT~~AVILQNN~~IT~~EFGTIIDWAPRGQFYHNCSSGQ  
 PGD-E1 (1) --RPGKPCPKKEIPKESKNT~~IT~~EVLVWEECVANS~~IT~~AVILQNN~~IT~~EFGTIIDWAPRGQFYHNCSSGQ  
 PGD-E2 (1) -----  
 PGD-E3 (1) -----  
 CONSENSUS (601) KFRPKGKPCPKKEIPKESKNT~~IT~~EVLVWEECVANS VILQNN~~IT~~EFGTIIDWAPRGQFYHNCSSGQ

GI\_4185940\_EMB\_CAA76880.1\_ (274) TQSCPSAQVSPA~~IT~~VDSDLTESLDKHKHKKLQSFYFWEWGEKGISTPRPKI~~IT~~SPVSGPEHPE 661  
 GI\_4185944\_EMB\_CAA76883.1\_ (274) TQSCPSAQVSPA~~IT~~VDSDLTESLDKHKHKKLQSFYFWEWGEKGISTPRPKI~~IT~~SPVSGPEHPE 720  
 GI\_4185948\_EMB\_CAA76886.1\_ (274) TQSCPSAQVSPA~~IT~~VDSDLTESLDKHKHKKLQSFYFWEWGEKGISTPRPKI~~IT~~SPVSGPEHPE  
 GI\_5931706\_EMB\_CAB56604.1\_ (168) TQSCPSAQVSPA~~IT~~VDSDLTESLDKHKHKKLQSFYFWEWGEKGISTPRPKI~~IT~~SPVSGPEHPE  
 ENV OF AB047240 (661) TQSCPSAQVSPA~~IT~~VDSDLTESLDKHKHKKLQSFYFWEWGEKGISTPRPKI~~IT~~SPVSGPEHPE  
 TRANSLATION OF E207TOP-LINK (31) -----  
 TRANSLATION OF ENV287-LINK (1) -----SDLTESLDKHKHKKLQSFYFWEWGEKGI  
 TRANSLATION OF T20.22A-23 (279) TQSCPSAQVSPA~~IT~~VDSDLTESLDKHKHKKLQSFYFWEWGEKGISTPRPKI~~IT~~SPVSGPEHPE  
 PGD-E1 (17) -----  
 PGD-E2 (1) -----  
 PGD-E3 (1) -----  
 CONSENSUS (661) TQSC SAQVSPA~~IT~~VDSDLTESLDKHKHKKLQSFYFWEWGEKGISTPRP IISPVSGPEHPE

GI\_4185940\_EMB\_CAA76880.1\_ (334) LWRLTVASHHIR~~IT~~WSGNQTL~~IT~~ETDRKPFY~~IT~~TIDLNSS~~IT~~TVPLQSC~~IT~~KPPYMLVVGNI~~IT~~VIKP 721  
 GI\_4185944\_EMB\_CAA76883.1\_ (334) LWRLTVASHHIR~~IT~~WSGNQTL~~IT~~ETDRKPFY~~IT~~TIDLNSS~~IT~~TVPLQSC~~IT~~KPPYMLVVGNI~~IT~~VIKP 780  
 GI\_4185948\_EMB\_CAA76886.1\_ (334) LWRLTVASHHIR~~IT~~WSGNQTL~~IT~~ETDRKPFY~~IT~~TIDLNSS~~IT~~TVPLQSC~~IT~~KPPYMLVVGNI~~IT~~VIKP  
 GI\_5931706\_EMB\_CAB56604.1\_ (228) LWRLTVASHHIR~~IT~~WSGNQTL~~IT~~ETRYRKP~~IT~~FY~~IT~~TIDLNSS~~IT~~TVPLQSC~~IT~~KPPYMLVVGNI~~IT~~VIKP  
 ENV OF AB047240 (721) LW-----R-----P-----  
 TRANSLATION OF E207TOP-LINK (31) -----  
 TRANSLATION OF ENV287-LINK (29) -----  
 TRANSLATION OF T20.22A-23 (339) LWRLTVASHHIR~~IT~~WSGNQTL~~IT~~ETDRKPFY~~IT~~TIDLNSS~~IT~~TVPLQSC~~IT~~KPPYMLVVGNI~~IT~~VIKP  
 PGD-E1 (17) -----  
 PGD-E2 (1) -----LNSS~~IT~~TVPLQSC~~IT~~KPC  
 PGD-E3 (1) -----  
 CONSENSUS (721) LW RI LNS LTVPLQSCVKP



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FIGURE 9 CONTD...

781 840

GI\_4185940\_EMB\_CAA76880.1\_ (394) DSQTITCENCRLTCTIDSTFNQHRILLVRAREGVWIPVSMRDPWEASPSVHILTEVLKG  
GI\_4185944\_EMB\_CAA76883.1\_ (394) DSQTITCENCRLTCTIDSTFNQHRILLVRAREGVWIPVSMRDPWETSPSIHTLTEVLKG  
GI\_4185948\_EMB\_CAA76886.1\_ (394) DSQTITCENCRLTCTIDSTFNQHRILLVRAREGVWIPVSMRDPWEASPSVHILTEVLKG  
GI\_5931706\_EMB\_CAB56604.1\_ (288) ASQTITCENCRLFTCTIDSTFNQHRILLVRAREGMWIPVSTDRPWEASPSIHTLTEILKG  
ENV OF AB047240 (727) -----DSTLEFGLLEIKL-----  
TRANSLATION OF E207TOP-LINK (31) -----  
TRANSLATION OF ENV287-LINK (29) -----  
TRANSLATION OF T20.22A-23 (399) DSQTITCENCRLTCTIDSTFNQHRILLVRAREGVWIPVSMRDPWEASPSVHILTEVLKG  
PGD-E1 (17) -----  
PGD-E2 (17) -----  
PGD-E3 (1) -----  
CONSENSUS (781) DST W I L

841 900

GI\_4185940\_EMB\_CAA76880.1\_ (454) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI  
GI\_4185944\_EMB\_CAA76883.1\_ (454) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI  
GI\_4185948\_EMB\_CAA76886.1\_ (454) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI  
GI\_5931706\_EMB\_CAB56604.1\_ (348) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNYWQKNSTRLWNSQSSI  
ENV OF AB047240 (739) -----  
TRANSLATION OF E207TOP-LINK (31) -----  
TRANSLATION OF ENV287-LINK (29) -----  
TRANSLATION OF T20.22A-23 (459) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI  
PGD-E1 (17) -----  
PGD-E2 (17) -----  
PGD-E3 (1) -----  
CONSENSUS (841)

901 960

GI\_4185940\_EMB\_CAA76880.1\_ (514) DQKLANQINDLRQTVIWMGDRMLSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH  
GI\_4185944\_EMB\_CAA76883.1\_ (514) DQKLANQINDLRQTVIWMGDRMLSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH  
GI\_4185948\_EMB\_CAA76886.1\_ (514) DQKLANQINDLRQTVIWMGDRMLSLEHRFQLQCDWNTSDFCITPQIYNESELHWDVRRH  
GI\_5931706\_EMB\_CAB56604.1\_ (408) DQKLANQINDLRQTVIWMGDRMLTLEHHFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH  
ENV OF AB047240 (739) -----  
TRANSLATION OF E207TOP-LINK (31) -----  
TRANSLATION OF ENV287-LINK (29) -----  
TRANSLATION OF T20.22A-23 (519) DQKLANQINDLRQTVIWMGDRMLSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH  
PGD-E1 (17) -----  
PGD-E2 (17) -----  
PGD-E3 (1) -----  
CONSENSUS (901)

961 1020

GI\_4185940\_EMB\_CAA76880.1\_ (574) LQGREDNLTLDISKLEKQIFEASKAHLNLPVPGTEAIAGVADGLANLNPVTWVKTIIGSTTI  
GI\_4185944\_EMB\_CAA76883.1\_ (574) LQGREDNLTLDISKLEKQIFEASKAHLNLPVPGTEAIAGVADGLANLNPVTWVKTIIGSTTI  
GI\_4185948\_EMB\_CAA76886.1\_ (574) LQGREDNLTLDISKLEKQIFEASKAHLNLPVPGTEAIAGVADGLANLNPVTWVKTIIGSTTI  
GI\_5931706\_EMB\_CAB56604.1\_ (468) LQGREDNLTLDISKLEKQIFEASKAHLNLPVPGTEAIAGVADGLANLNPVTWIKTIRSTMI  
ENV OF AB047240 (739) -----  
TRANSLATION OF E207TOP-LINK (31) -----  
TRANSLATION OF ENV287-LINK (29) -----  
TRANSLATION OF T20.22A-23 (579) LQGREDNLTLDISKLEKQIFEASKAHLNLPVPGTEAIAGVADGLANLNPVTWVKTIIGSTTI  
PGD-E1 (17) -----  
PGD-E2 (17) -----  
PGD-E3 (1) -----  
CONSENSUS (961)

1021 1081

GI\_4185940\_EMB\_CAA76880.1\_ (634) INLILILVCLFCLLLVCRCTQQLRRSDHRRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV  
GI\_4185944\_EMB\_CAA76883.1\_ (634) INLILILVCLFCLLLVCRCTQQLRRSDHRRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV  
GI\_4185948\_EMB\_CAA76886.1\_ (634) INLILILVCLFCLLLVCRCTQQLRRSDHRRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV  
GI\_5931706\_EMB\_CAB56604.1\_ (528) INLILIVCLFCLLLVCRCTQQLRRSDIENG-----  
ENV OF AB047240 (739) -----  
TRANSLATION OF E207TOP-LINK (31) -----  
TRANSLATION OF ENV287-LINK (29) -----  
TRANSLATION OF T20.22A-23 (639) INLILILVCLFCLLLVCRCTQQLRRSDHRRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV  
PGD-E1 (17) -----  
PGD-E2 (17) -----  
PGD-E3 (1) -----  
CONSENSUS (1021) -----RCTQQLRRSDHRRER-----  
RCTQQLRRSD